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                                                                            Local Similarity
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                     aaaaccacagtaggaaaaa 117
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 444 Std Error: 0.00
Seq primer: 40m13 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2286482.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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similar to
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19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ph.D.
                                                                                                                                                 /note-"Organ: breast; Vector: pAMP10; mRNA made from normal breast ductal tissue, cDNA made by oligo-dr priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

88 c 77 g 131 t
                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1191644"
/clone_lib="NCI_CGAP_Br4"
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1 NCI_CGAP_Br4
o contains Alu
                                                                                                                                                                                                                                         /tissue_type="normal ductal tissue"
/lab_host="DH10B"
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Homo sapiens cDNA clone IMAGE:1191644
repetitive element;, mRNA secuence
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Eukaryota, Metazoa; Chordata, Craniata; Vertebramanmalia; Eutheria; Primates; Catarrhini; Homin: 1 (bases 1 to 470) 2hao,S., Adams,M.D., Nyerman,W., Malek,J., Shizu Venter,J.C.
Use of BAC End Sequences from CalTech Libraries Map Building
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HS_3055_K1_F05_MF CIT Approved Human Genomic Sperm Library
Homo sapiens genomic clone Plate=3055 Col=9 Row-K, genomic
survey sequence.
Ad100432
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High Throughput Sequencing Center
University of Washington
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1 (bases z to 37)

Mahairas G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Kelley A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ai
                                                                                                                                                                                                                                           AQ352552 470 bp DNA CITBI-E1 Homo sapiens genomic survey sequence.
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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/db_xref="taxon:9606"
/clone="plate=3055 Col=9 R
/clone_lib="CIT Approved H
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: sperm; Vector:
E-Coli DH10B"
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clone 254101,
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Adams,M.D. and
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Sequencing vector: M.3; 100%
Sequencing vector: M.3; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version—0, 990319
Consensus quality: 16884 bases at least Q40
Consensus quality: 16875 bases at least Q30
Consensus quality: 16940 bases at least Q30
Consensus quality: 16940 bases at least Q30
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1 (bases 1 to 172191)
Waterston, R. H.
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Submitted (04-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 6318, USA
On Apr 16, 2000 this sequence version replaced accommons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center Washington University Genome Sequencing Center Center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
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Insert size: 170591;
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                                                                                                                          26484: contig
26584: gap of
34254: contig
                                                                                                                                                                     21936: contig of 4966 bp in
22036: gap of unknown length
36484: contig of 4448 bp in
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of unknown length of 7670 bp in the contig of 7670 bp in the contig of 7962 by the gap of unknown length of manner of unknown length of manner of unknown length of the contig of the co
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1 (bases 1 to 2573)
Martin, C.H., Bondoc, M.M., Chiang, A., Cloutier, T., Davis, C.A., Ericsson, C.L., Jaklevic, M.A., Kim, R. J., Lee, M.T., Li, M., Kayeda, C.A., Stelert-El Kheir, A. and Palazzolo, M.J. Sequencing of the interleukin gene cluster of homo sapiens inpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                  This subclone overlaps H22 8_c11 and H22 5_c7. The P1, from which this subclone is derived, i sequence submitted by:
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Homo sapiens (tissue library:
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Homo sapiens (subclone
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human. 96 Homo sapiens Eukaryota; Metazoa; C Primates; Catarrhini;	RESULT 34 HSAJ1685/c HSAJ1686/c H	Qy 148 cctaaaacttaaagt 162 	Ouery Match 40.8%; Score 75; DB 10; Length 3088; Best Zocal Similarity 100.0%; Pred. No. 5.9e-29; Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 88 agcacacatggcacatgtatacatatgtaacafaacctgcacattgtgcacatgtac 147	Source 'Jaganism-"Homo sapiens' 'Ch_xref="taxon:9606" 'Ch_xref="taxon:9606" Ch_xref="taxon:9606" Ch_xref="taxon:9606" Chissue_lib="Subclones in pot2 from P1 clong H22" BASE COUNT 986 a 567 c 598 g 967 t ORIGIN		Mayeda,C.A., Pacleb,J.M., Palazzolo,M.J., Patel,S.G., Santos,R.F., Bubramanian,S., Tordilla,N.E., Truong,V., Verhofstadt-Gann,K., Wan,K.H., Whitelaw,K.R., Yee,A., Yeh,K.T. and Yu,C. TITLE Sequencing of the interleukin gene Cluster of homo sapiens JOURNAL Jnpublished (1995) Sequence submitted by: Human Genema Conter	CREARISM HOMO Sapiens Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Mampalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 3088) ROTHORS Arcaina, T. T., Bondoc, M.M., Chiang, A., Critz, P.A., Davis, C.A., Doyle, C.M., Ericsson, C.L., Gunning, R.M., Houstow, K.A., Jakleyac, M.A., Jimenbz, L.A., Kadner, K.E., Kim, S.F., Kowtha, K.V., Lee, K.K., Li, M., Lindquist, K.J., Machrus, M.B., Martin, C.H.,	HUM22 Homo L7704 L7704 Inter Homo	Oy 148 cctaaaacttaaagt 162	Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 88 agcaccaaccaaccaggtatacatatgtaaccagaacctgcacattgtgcacatgtac 147
/gene="NKGZE" /number=4 9835, .3935 /gene="NKGZE"	intron 1557. 2102 /gene="N#67E" /number=3 exon 2103. 2257 gene="N#62E" /number=4 intron 2258. 3834	/gene- /numbe 1512. /gene-	QCGSSRIIRRGFIMLTRLVLNS" 1nzfon 233. 631 /gene="NKG2E" /number=1 /number=2 /number=2 /number=7 /number=7 /number=7 /number=7 /number=1	/protein_1d="caa04923:1" /bb_xref="GI:2900861" /db_xref="GI:990861" /db_xref="WISS-PROT:007444" /translation="MNKQRCTFSEVSLAQDPKPQQRKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPQQRKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPQQRKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPQGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKPGGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDPKGIKPKGNKSSISGTEQEIFQVELN /translation="MNKQRCTFSEVSLAQDFKGNKSSISGTEQEIFQVELN" /translation="MNKQRCTFSEVSLAQDFKGNKSSISGTEQEIFQUELN" /translation="MNKQRCTFSEVSLAQDFKGNKSSISGTEQEIFQUELN" /translation="MNKQRCTFSEVSLAQDFKGNKSSISGTEQEIFQUELN" /translation="MNKQRCTFSEVSLAQDFKG	/gene="NKGZE" 1. 8230 /gene="NKGZE" 23,632730,15121556,21032257,38353935, CDS	exon /map="12p" 1. 23 /map="NKG2E" /gene="NKG2E" /number=1 /number=1 /oin(1. 232,632. 730,1522. 1556,2103. 2257,3835. 3935, 4808. 4898,7986. 82907	RES Location/Qualifiers RES Location/Qualifiers source /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="12" /clone="from PAC clone D21184"	REMARK Extratum: [[published extatum appears in immunogenetics 1994;40(4):318]] REFERENCE 3 (bases 1 to 9555) AUTHORS Glienke, J., Sobanov f., Brostjan, C., Steffens, C., Nguyen, C., Lehrach, H., Hofery E., and Francis, F. TITLE the genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex JOURNAL Immunogenetics 48 (3), 163-173 (1998) MEDLINE 98350122	ch, F.A	ENCE HORS LE RNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean nodulin-26 gene encoding a channel protein is expressed only in the infected cells of nodules and is regulated differently in roots of homologous and heterologous plants plant Cell 5 (7), 781-794 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M94764.1 GI:170029
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                                                                                                                                                                                                                                                                                                                                                                                                                     Edkaryota; Metazoa; Chordata; Cyaniata; Vertebrata; Euteleoskomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 71801)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
            Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bed Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, Campopiano, A., Castle, A., Choepel, Y., Colangelo, W., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Filchu Dodge, S., Domino, M., Doyle, M., Ferreira, P., Filchu
                                                                                                                                                                                                                                                                                                   2 (bases 1 to 71801
Birren, B., Linton, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hope sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome
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824 c 877 g 21
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Pred. No.
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McGurk, A., McKernan, K.,
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   McPheeters, R.,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-MAR/2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome
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Contact: sequence_submissions@genome.wi.mit.edu
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10258 10260 1000
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747 846: gap of 100 bp
847 1601: contig of 755 bp in length
1602 1701: gap of 100 bp
1702 2462: cont/19 of 767
                                                                                                                                                                                                                                                                                                                                                10258 10999; contig of 742 bg
11000 11099; gap of 100 bg
11100 11854; contig of 755 bg
11855 11954; gap of 100 bp
11855 12717; contig of 63 bg
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14424 14523: gap
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1635: contig of 765 bp in
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16435: contig of 747 bp in
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398: gap of 100
10157: contig of 764 k
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5874: contig of 763 bp
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1562: contig of 758 bp in
gap of 100 hr
                                                                                                                                                                                                                                                       68: contig
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O'Connor,T., O'Donnell,P.,
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RESULT 1
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score greater than or equal to the score of the result being prin
and is derived by analysis of the total score distribution.
AA493099
ng96d01.s1
similar to
                                                                                                                             Match
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9b_98614:*
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9b_98815:*
9b_98817:*
9b_98819:*
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162 bp mRNA EST 19-AUG-1997 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:942625 contains Alu repetitive element; contains element MER9
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353
667
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AQ11411 CIT HSP-

AQ635928 RPCI-11.

A1858468 w138903...

AA847029 0009a01...

AQ475892 CITE HSP-

AQ316521 CIT HSP-

AQ103431 HS-3665.
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AW302950 xr58d12
AI144036 qx63b02
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AQ277318 CITB1-E1-
AQ692714 HS_5415-A
AQ174494 tr17f04.x
AQ167057 HS_3151_B
AQ799581 HS_4507_X
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Best Local Similarity 100.0%;
Matches 72; Conservative
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   Eukaryota; Mgtazoa; Chc
Eukaryota; Mgtazoa; Chc
Mammalia; Edtheria; Pri
1 (bases 1 to 300)
Hillier,L', Clark,N., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 451 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 153.

Location/Qualifiers
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                                                                                                                  W07101 300 bp MRNA EST 25-APR-1996 2493d06.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone finage:300107 5' similar to contains alu repetitive element;contains element merzz repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
On Jan 14, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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1 (bases 1 to 162)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                            W07101.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:942525"
/clone_1b="NCL:CGAP_Thyl"
/tissue_type="thyroid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pAMP10; mRNA made from invasive thyroid tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                               GI:1281/114
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Primates;
                                 Chordata;
Primates;
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       Dubuque,
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                               Crandata; Vertebrata; Eutelgostomi; Caparrhini; Hominidae; Homo.
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. 6.3e-24;
ches 0;
         Elliston, K.,
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          Hawkips, M.,
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9b_9ss14: *
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9b_9ss17: * *
9b_9ss18: * * *
9b_9ss18: * *
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AQ322354
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AW328446 G802f03.y
AI277373 gm54c07.x
AI439816 t156d10.x
AI439840 gm53c11.y
AI435639 th47h01.x
AA490602 aA47768.s
AA480162 ne30b07.s
                                                                                                                                                                                                                                                                       AA507837 ng86d05.s
AA196390 zp99b10.s
AQ747348 HS_5536_A
F34489 HSPD29378 H
                                                                                                                                                     AA993227 0102268.s
AQ114141 CITY-HSP-2
AQ635928 KPCI-11-4
AA471377/PMY1149 K
AA472377 nq07909.s
T41332 phla6_19/IT
                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ180060 HS_3204_I
AQ277318 CITBI-E1
AQ692714 HS_5415
AI744949 tr17f04/J
AQ167057 HS_3151_I
AQ799581 HS_4507
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76792 RPTTTCC
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Matches 119;
                                                                 ORGANISM
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                                                                                                                                                                                                                                                                              atotacccacctcagtctccccaaagtgctgggattacaggtgtgagagagccgcacccag 392
                                                                                                                                                                                                                                                               ATCTACCCACCTCAGTCTCCCAAAGTGCTGGGATTACAGGTGTGAGAGACCGCACCCAG
      Eukaryoia Metazoa; Chordata; Craniata; Verrebraca; Eutele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Danes 1 to 300)
Miller L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                               w07101 300 bp mRNA za93dO&/r1 Soares_fetal_lung_NbHL19W Hemo sapiens cDNA clone IMAGE:300107 5' similar to containe Alu repetitive element; cc exement MER22 repetitive element; cr
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 451 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 153.
Location/Qualifiers
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Unpublished (1997)
On Jan 14, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
1 (bases 1 to 162)
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="thyroid"
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Primates;
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pred. No. 9.2e-46;
0; Mismatches 0;
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                                                      Euteleostomi;
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Gaps

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